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OM nucleic - nucleic search, using sw model

Run on: March 29, 2003, 19:47:07 ; Search time 47.5859 Seconds
(without alignments)
7950.588 Million cell updates/sec

Title: US-09-988-971-1_COPY_517_684

Perfect score: 168
Sequence: 1 gccacagccgtgcccctg99.....gctccacgctgcacaaagtc 168

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1984.DAT.*
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8: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1990.DAT.*
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13: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA1993.DAT.*
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21: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneeq/geneeqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	168	100.0	737 24	Mouse MARS short i
2	168	100.0	786 24	Human modulator of
3	168	100.0	2049 23	DNA encoding novel
4	166.4	99.0	837 21	Human ORF2757
5	166.4	99.0	1183 24	Human CDNA encodin
6	124.8	74.3	1348 24	Human modulator of
7	80.8	48.1	211 23	DNA encoding novel
8	43.6	26.0	2298 24	Human CDNA differe
9	39	23.2	2109 22	DNA encoding molec

10	39	23.2	2665 24	ABK83738	Human CDNA differe
11	39	23.2	2665 24	ABK65189	Lung cancer relate
12	34.4	20.5	2032 21	AAZ46491	PKA substrate, Src
13	33	19.6	577 22	ABA13398	Probe #9864 for ge
14	33	19.6	577 22	AA144415	Probe #13101 used
15	33	19.6	3311 18	AA770377	Cytoskeleton 1. Homo
16	33	19.6	3311 24	ABK84102	Human CDNA differe
17	33	19.6	3311 24	ABO66425	Human cytohesin-1
18	33	19.6	6933 23	ABK51514	DNA encoding novel
19	32.2	19.2	183 24	ABK61214	Human nucleotide f
20	32.2	19.2	1416 24	ABK61215	Human nucleotide f
21	32.2	19.2	1542 24	ABK61216	Human nucleotide f
22	32.2	19.2	1926 24	ABK83340	Human CDNA differe
23	32.2	19.2	2015 24	ABK83339	Human CDNA differe
24	32.2	19.2	2015 24	ABK66673	Human cancer relate
25	32.2	19.2	2350 22	AAK53035	Human polynucleoti
26	31.6	18.8	6855 24	AAK516827	Human T-cybe calci
27	31.6	18.8	48657 24	ABK51628	Human T-cybe calci
28	31.4	18.7	6232 13	AAQ29269	Human transporter
29	31.2	18.6	123 22	ABA40888	Human calcium chan
30	31.2	18.6	123 22	AA157031	Probe #19354 for g
31	31.2	18.6	123 22	AAK89277	Human brain T calc
32	31.2	18.6	1574 21	AAZ86794	Human protein kina
33	31.2	18.6	1574 22	AAZ81845	Human protein kina
34	31	18.5	3663 18	AAZ72520	Human protein kina
35	30.8	18.3	3401 22	AAK52257	Embryonic stem cel
36	30.8	18.3	3401 22	AAK56130	Human DNA encoding
37	30.8	18.3	3401 22	AAK72415	Human PRO247 CDN
38	30.8	18.3	3401 24	ABK55580	Human angiogenesis
39	30.8	18.3	3401 24	ABK88091	Human PRO247 CDN
40	30.8	18.3	3401 24	ABK33597	CDNA encoding huma
41	30.8	18.3	14705 23	AAK59523	Protonibacterium
42	30.6	18.2	160 20	AAK80580	Kidney injury asso
43	30.4	18.1	621 24	ABK34574	Human CDNA encodin
44	30.4	18.1	3336 24	ABK84672	Human CDNA differe
45	30.4	18.1	13336 23	AAK59554	Protonibacterium

ALIGNMENTS

RESULT 1	AA144090	standard; CDNA; 737 BP.
ID	AA144090	
XX	AA144090;	
AC	AA144090;	
XX		
DT	03-OCT-2002	(first entry)
XX		
DE	Mouse MARS short isoform protein coding sequence.	
XX		
KM	Mouse; gene; ss; gene therapy; modulator of antigen receptor signalling;	
KM	MARS; tumor suppressor gene; Src-like adaptor protein; SLAP;	
KM	myeloid malignancy; acute myelogenous leukemia; autoimmune disorder;	
KM	immunopression; myeloproliferative disorder; breast cancer.	
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..633
FT		/*tag= a
FT		/product= "Mouse MARS short isoform protein"
PN	MO200242452-A2.	
XX		
PD	30-MAY-2002.	
XX		
PF	26-NOV-2001; 2001MO-CA01662.	
XX		
PR	27-NOV-2000; 2000CA-2324663.	
PA		
XX	(HOSP-) HOSPITAL FOR SICK CHILDREN.	

PI Mcglade JC, Loreto MP;
 XX
 DR WPI; 2002-566564/60.
 DR P-PSDB; AAO15458.
 XX
 PT New isolated modulator of antigen receptor signalling protein or its
 PT fragment, useful for treating malignant disorders such as myeloid
 PT malignancies, autoimmune disorders and myeloproliferative disorders -
 XX
 PS Claim 9; Page 77; 110pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of modulator
 CC of antigen receptor signalling (MARS) proteins. The MARS protein is a
 CC putative tumour suppressor gene and exhibits structural and sequence
 CC similarity to the Src-like adaptor protein (SLAP). The MARS DNA and
 CC protein sequences of the invention are useful for the treatment of
 CC myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune
 CC disorders, immunosuppression, myeloproliferative disorders and
 CC malignancies related to the de-regulation of tyrosine kinases (e.g.
 CC breast cancer). The present cDNA sequence encodes a mouse MARS protein.
 CC
 SQ Sequence 737 BP; 152 A; 219 C; 218 G; 148 T; 0 other;
 Query Match 100.0%; Score 168; DB 24; Length 737;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCCACAGCCGTCGCGCCCTGGGCACTTCCCGCAGGTGACCCGCGCAGCTGCTGAGA 60
 DB 103 GCCACAGCCGTCGCGCCCTGGGCACTTCCCGCAGGTGACCCGCGCAGCTGCTGAGA 162
 QY 61 CTCGGGAGCATTGACCATGCTCTGAGATGAGAGACTGTGACGAGTCTGTGAA 120
 DB 163 CTCGGGAGCATTGACCATGCTCTGAGATGAGAGACTGTGACGAGTCTGTGAA 222
 QY 121 GTCTCAGGCAAGAGATTAACATCCCAAGCTCCAGCTGCGCAAAATC 168
 DB 223 GTCTCAGGCAAGAGATTAACATCCCAAGCTCCAGCTGCGCAAAATC 270

RESULT 2
 AAL44089
 ID AAL44089 standard; cDNA; 786 BP.
 XX
 AC AAL44089;
 XX
 DT 03-OCT-2002 (first entry)
 XX
 DE Human modulator of antigen receptor signalling protein coding sequence.
 XX
 KW Human; gene; ss; gene therapy; modulator of antigen receptor signalling;
 KW MARS; tumour suppressor gene; Src-like adaptor protein; SLAP;
 KW myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder;
 KW immunosuppression; myeloproliferative disorder; breast cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..786
 FT /*tag= a
 FT /product= "Human MARS protein"
 XX
 PN WO200242452-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 26-NOV-2001; 2001WO-CA01662.
 XX
 PR 27-NOV-2000; 2000CA-2324663.
 XX
 PA HOSP-1 HOSPITAL FOR SICK CHILDREN.
 XX
 PI Mcglade JC, Loreto MP;

XX
 DR WPI; 2002-566564/60.
 DR P-PSDB; AAO15457.
 XX
 PT New isolated modulator of antigen receptor signalling protein or its
 PT fragment, useful for treating malignant disorders such as myeloid
 PT malignancies, autoimmune disorders and myeloproliferative disorders -
 XX
 PS Claim 12; Page 75; 110pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of modulator
 CC of antigen receptor signalling (MARS) proteins. The MARS protein is a
 CC putative tumour suppressor gene and exhibits structural and sequence
 CC similarity to the Src-like adaptor protein (SLAP). The MARS DNA and
 CC protein sequences of the invention are useful for the treatment of
 CC myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune
 CC disorders, immunosuppression, myeloproliferative disorders and
 CC malignancies related to the de-regulation of tyrosine kinases (e.g.
 CC breast cancer). The present cDNA sequence encodes a human MARS protein.
 CC
 SQ Sequence 786 BP; 162 A; 234 C; 231 G; 159 T; 0 other;
 Query Match 100.0%; Score 168; DB 24; Length 786;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCCACAGCCGTCGCGCCCTGGGCACTTCCCGCAGGTGACCCGCGCAGCTGCTGAGA 60
 DB 103 GCCACAGCCGTCGCGCCCTGGGCACTTCCCGCAGGTGACCCGCGCAGCTGCTGAGA 162
 QY 61 CTCGGGAGCATTGACCATGCTCTGAGATGAGAGACTGTGACGAGTCTGTGAA 120
 DB 163 CTCGGGAGCATTGACCATGCTCTGAGATGAGAGACTGTGACGAGTCTGTGAA 222
 QY 121 GTCTCAGGCAAGAGATTAACATCCCAAGCTCCAGCTGCGCAAAATC 168
 DB 223 GTCTCAGGCAAGAGATTAACATCCCAAGCTCCAGCTGCGCAAAATC 270

RESULT 3
 AAS74750
 ID AAS74750 standard; cDNA; 2049 BP.
 XX
 AC AAS74750;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #10554.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYTE-) HYTEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG10563.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess

PT biodiversity -
XX Claim 1; SEQ ID No 10554; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIGO
XX at ftp.wigo.int/pub/published_pct_sequences.
XX
XX Sequence 2049 BP; 479 A; 573 C; 551 G; 443 T; 3 other:
XX
XX Query Match 100.0%; Score 168; DB 23; Length 2049;
XX Best Local Similarity 100.0%; Pred. No. 3e-40;
XX Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCCACAGCCGCTGGCCCTGGGAGTTTCCCGGAGGTGCGCCGCGAGCTGCTGCTGAGA 60
XX |
XX 1067 GCCACAGCCGCTGGCCCTGGGAGTTTCCCGGAGGTGCGCCGCGAGCTGCTGAGA 1126
XX |
XX 61 CTCGGGGAGCCATTGACCATCTGCTCTGAGATGAGATGCTGAGACGGTCTGTGAA 120
XX |
XX 1127 CTCGGGGAGCCATTGACCATCTGCTCTGAGATGAGATGCTGAGACGGTCTGTGAA 1186
XX |
XX 121 GTCTCAGGAGAGAGTAAATCATCCCGAGCGTCCACCGTGGCCAAAGTC 168
XX |
XX 1187 GTCTCAGGAGAGAGTAAATCATCCCGAGCGTCCACCGTGGCCAAAGTC 1234
XX |
XX
XX RESULT 4
XX AACT7202
XX ID AACT7202 standard; cDNA; 837 BP.
XX AC AACT7202;
XX XX
XX DT 08-FEB-2001 (first entry)
XX DE Human ORFX ORF2757 polynucleotide sequence SEQ ID NO:5113.
XX XX
XX Human; open reading frame; ORFX; detection; cytosstatic; hepatotropic;
XX vulnarary; antipsoptic; antiparkinsonian; nocrotic; neuroprotective;
XX anticonvulsant; osteopathic; antitachytic; immunosuppressant; cardiac;
XX immunosimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
XX hypotensive; dermatological; immunosuppressive; antihypertensive;
XX antiviral; antibacterial; antifungal; antineuritic; antitumor;
XX antitubercular; gene therapy; cancer; proliferative disorder; hypertension;
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
XX cardiovascular disease; diabetes mellitus; hypochyroidism; SCID; AIDS;
XX cholesterol ester storage; systemic lupus erythematosus; infection;
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
XX bone damage; cartilage damage; antinflammatory disease; coagulation;
XX thrombosis; contraceptive; 58.
XX
XX OS Homo sapiens.
XX XX
XX PN M0200058473-A2.
XX
XX
XX PD 05-OCT-2000.
XX PF 31-MAR-2000; 2000MO-US08621.
XX PR 31-MAR-1999; 99US-0127607.
XX PR 02-APR-1999; 99US-0127636.
XX PR 05-APR-1999; 99US-0127728.
XX PR 30-MAR-2000; 2000US-0540763.
XX PA (CURA) CURAGEN CORP.
XX PI Shimkete RA, Leach M;
XX XX
XX WPI: 2000-602362/57.
XX P-PSDB; AAB42993.
XX
XX Claim 5, Page 4692-4693; 5507bp; English.
XX
XX AACT7446 to AACT7606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytosstatic; hepatotropic; vulnarary;
XX antipsoptic; antiparkinsonian; nocrotic; neuroprotective;
XX osteopathic; anticonvulsant; antitachytic; immunosuppressant;
XX immunosimulant; cardiac; thrombolytic; coagulant; vasotropic;
XX antidiabetic; hypotensive; dermatological; immunosuppressive;
XX antinflammatory; antibacterial; antiviral; antifungal; antineuritic;
XX antitubercular; antitumor. The sequences can be used for determining
XX the presence of or predisposition to, or preventing or treating
XX pathological conditions associated with an ORFX-associated disorder. The
XX nucleic acids can be used to express ORFX proteins in gene therapy
XX vectors. The proteins and nucleic acids may be used to treat cancers,
XX proliferative disorders, neurodegenerative disorders, osteoarthritis,
XX graft vs host disease, cardiovascular disease, diabetes mellitus,
XX hypertension, hypochyroidism, cholesterol ester storage, systemic lupus
XX erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
XX bacterial or fungal infection, malaria, autoimmune disorders, asthma,
XX allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
XX nocturnal haemoglobinuria, antinflammatory disease, to enhance
XX coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX Sequence 837 BP; 176 A; 254 C; 245 G; 160 T; 2 other:
XX
XX Query Match 99.0%; Score 166.4; DB 21; Length 837;
XX Best Local Similarity 99.4%; Pred. No. 7.3e-40;
XX Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 GCCACAGCCGCTGGCCCTGGGAGTTTCCCGGAGGTGCGCCGCGAGCTGCTGAGA 60
XX |
XX 64 GCCACAGCCGCTGGCCCTGGGAGTTTCCCGGAGGTGCGCCGCGAGCTGCTGAGA 123
XX |
XX 61 CTCGGGGAGCCATTGACCATCTGCTCTGAGATGAGATGCTGAGACGGTCTGTGAA 120
XX |
XX 124 CTCGGGGAGCCATTGACCATCTGCTCTGAGATGAGATGCTGAGACGGTCTGTGAA 183
XX |
XX 121 GTCTCAGGAGAGAGTAAATCATCCCGAGCGTCCACCGTGGCCAAAGTC 168
XX |
XX 184 GTCTCAGGAGAGAGTAAATCATCCCGAGCGTCCACCGTGGCCAAAGTC 231
XX |
XX
XX RESULT 5
XX ABBK1465
XX ID ABBK1465 standard; cDNA; 1183 BP.
XX AC ABBK1465;
XX XX
XX DT 18-JUN-2002 (first entry)
XX DE Human cDNA encoding protein NOV13.
XX
XX

XX Human; gene; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis;
 KW cell signal processing disorder; metabolic pathway modulation disorder;
 KW diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer;
 KW uterus cancer; immune response; graft-versus-host disease;
 KW acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease;
 KW hypertension; congenital heart defects; multiple sclerosis; inflammation;
 KW Albritight hereditary osteodystrophy.
 XX Homo sapiens.
 OS
 PN MO200216599-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 27-AUG-2001; 2001WO-US26510.
 XX
 PR 25-AUG-2000; 2000US-228191P.
 PR 08-FEB-2001; 2001US-267300P.
 PR 20-FEB-2001; 2001US-269961P.
 PR 20-MAR-2001; 2001US-277337P.
 XX
 PA (CURA-) CURAGEN CORP.
 PA (CORT-) COR THERAPEUTICS INC.
 PI Burgess CE, Conley PB, Grosse WM, Hart M, Kekuda R, Shinkets RA;
 PI Szytek KA, Szekeres ES, Tomlinson JF, Topper JN, Yang R;
 XX
 DR MPI: 2002-280937/32.
 DR P-PSDB; AAU91308.
 XX
 PT New polypeptides for treating or preventing a disorder associated with
 PT them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers -
 PS
 PS Claim 1; Page 98; 263pp; English.
 XX
 CC The invention relates to an isolated polypeptide (NOVX) a mature
 CC form of NOVX, a NOVX variant (differing by no more than 15%), the
 CC nucleotide encoding NOVX (or its complement, fragment or variant),
 CC NOVX is NOVX-14, 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic
 CC acid encoding it and antibody against it, are useful for treating or
 CC preventing (e.g. by gene therapy) a NOVX-associated disorder in humans,
 CC e.g. cardiomyopathy, atherosclerosis, a disorder related to cell signal
 CC processing and metabolic pathway modulation, diabetes or cancers. The
 CC NOVX polypeptide and nucleic acids are also useful for determining the
 CC presence of predisposition to the diseases. The NOVX nucleic acid and
 CC polypeptide are especially useful in therapeutic or prophylactic
 CC applications for disorders associated with aberrant NOVX expression or
 CC activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or
 CC uterus cancer), immune response, graft-versus-host disease, acquired
 CC immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension,
 CC congenital heart defects, multiple sclerosis, inflammation or Albritight
 CC hereditary osteodystrophy and many other diseases listed in the
 CC specification. The DNA encoding the protein is useful in gene therapy
 CC for treating the conditions. This is also useful in detection assays,
 CC chromosome mapping, tissue typing, diagnostic or prognostic assays, or
 CC for developing a powerful assay system for functional analysis of
 CC various human disorders, as well as in diagnostic applications. The
 CC present sequence encodes a NOVX protein.
 XX
 SQ Sequence 1183 BP; 251 A; 359 C; 333 G; 240 T; 0 other;
 Query Match 99.0%; Score 166.4; DB 24; Length 1183;
 Best Local Similarity 99.4%; Pred. No. 7.8e-40;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCCACAGCCGCTGCTGCGGAGATTCCCGCAGGTGCGCCGCGAGCTGTCTGTGAGA 60
 DB 500 GCCACAGCCGCTGCTGCGGAGATTCCCGCAGGTGCGCCGCGAGCTGTCTGTGAGA 559
 QY 61 CTCGGGAGGCGATTGACATCATCTCTGAGAGATGAGACTGTGTGAGATGAGTCTGTGAA 120
 DB 560 CTCGGGAGGCGATTGACATCATCTCTGAGAGATGAGACTGTGTGAGATGAGTCTGTGAA 619

QY 121 GTCTCAGCAGAGAGATTAACATCCCGAGCTCCAGCTGCGCAAAATGTC 168
 DB 620 GTCTCAGCAGAGAGATTAACATCCCGAGCTCCAGCTGCGCAAAATGTC 667
 RESULT 6
 ID AAL44087 standard; cDNA; 1348 BP.
 XX
 AC AAL44087;
 XX
 DT 03-OCT-2002 (first entry)
 XX
 DE Mouse modulator of antigen receptor signalling protein coding sequence.
 XX
 KW Mouse; gene; ss; gene therapy; modulator of antigen receptor signalling;
 KW MARS; tumour suppressor gene; Scr-like adaptor protein; SLAP;
 KW myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder;
 KW immunosuppression; myeloproliferative disorder; breast cancer.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT 282..1061
 FT CDS /*tag= a
 FT /product= "Mouse MARS protein"
 XX
 PN MO200242452-A2.
 PD 30-MAY-2002.
 XX
 PF 26-NOV-2001; 2001WO-CA01662.
 PR 27-NOV-2000; 2000CA-2324663.
 XX
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
 PI Mcglade JC, Loreto MP;
 XX
 DR MPI: 2002-565564/60.
 DR P-PSDB; AA015456.
 XX
 PT New isolated modulator of antigen receptor signalling protein or its
 PT fragment, useful for treating malignant disorders such as myeloid
 PT malignancies, autoimmune disorders and myeloproliferative disorders -
 PS
 PS Claim 10; Fig 1A; 110pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of modulator
 CC of antigen receptor signalling (MARS) proteins. The MARS protein is a
 CC putative tumour suppressor gene and exhibits structural and sequence
 CC similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and
 CC protein sequences of the invention are useful for the treatment of
 CC myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune
 CC disorders, immunosuppression, myeloproliferative disorders and
 CC malignancies related to the de-regulation of tyrosine kinases (e.g.
 CC breast cancer). The present cDNA sequence encodes a mouse MARS protein.
 XX
 SQ Sequence 1348 BP; 324 A; 385 C; 362 G; 277 T; 0 other;
 Query Match 74.3%; Score 124.8; DB 24; Length 1348;
 Best Local Similarity 83.9%; Pred. No. 1.7e-27;
 Matches 141; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 QY 1 GCCACAGCCGCTGCTGCGGAGATTCCCGCAGGTGCGCCGCGAGCTGTCTGTGAGA 60
 DB 381 GTCAACACTGTGTGCTGCGGAGATTCCCGCAGGTGCGCCGCGAGCTGTCTGTGAGA 440
 QY 61 CTCGGGAGGCGATTGACATCATCTCTGAGAGATGAGACTGTGTGAGATGAGTCTGTGAA 120
 DB 441 CTCGGGAGGCGATTGACATCATCTCTGAGAGATGAGACTGTGTGAGATGAGTCTGTGAA 500

CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC peridontal disease, also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and MS is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 2298 BP; 645 A; 564 C; 576 G; 513 T; 0 other;

Query Match 26.0%; Score 43.6; DB 24; Length 2298;
 Best Local Similarity 58.5%; Pred. No. 0.0023;
 Matches 76; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

OY 39 CCGGCGGAGCTGTGCTGAGACTCGGAGCCATTCCTCTGAGATGAGA 98
 DB 531 CCGGAGCACTGTCTTTCAAGAAAGAGAAAGTCTGAGAGATGAGA 590
 OY 99 CTGTGACCGGTCTGTCTGAAGTCTAGGAGAGATTAATATCCCAAGCTCACT 158
 DB 591 ATGTGGAAGAGCAAGTCCCTTTTAAACAAAAAGAGGCTTATCCCGAGCACTATGT 650
 OY 159 GGGCAAAAGTC 168
 DB 651 GGGCAAACTC 660

RESULT 9
 AAS02049
 ID AAS02049 standard; cDNA; 2109 BP.

AC AAS02049;

DT 16-JUL-2001 (first entry)

DE DNA encoding molecule for disease detection and treatment; mdc14.

XX Human; mdc14; gene therapy; adenosine deaminase deficiency;
 KW ADA; severe combined immunodeficiency syndrome; cystic fibrosis;
 KW thalassemia; familial hypercholesterolaemia; haemophilia; factor VIII;
 KW factor IX; cancer; cell proliferation; parasite; human retrovirus; HIV;
 KW hepatitis B; hepatitis C; Candida albicans; Plasmodium falciparum;
 KW Paracoccidioides brasiliensis; Trypanosoma brasiliensis; ss.

OS Homo sapiens.

PN WO200123538-A2.

PD 05-APR-2001.

XX 22-SEP-2000; 2000MO-US26085.

XX 28-SEP-1999; 99US-0155565.

XX 30-NOV-1999; 99US-0168197.

PA (INCYTE) INCYTE GENOMICS INC.

PI Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
 PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shan P, Chalup MS;
 PI Hillman JL, Jones AL, Yu Y, Greenwalt LB, Panzer SR;
 PI Roseberry AM, Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK;
 PI Amesley S, Fong WT;
 DR WPI: 2001-258131/26.

PT Purified disease treatment and detection molecule polynucleotides and
 PT polypeptides, useful for providing diagnostic assays and gene therapy -

PS Claim 1; Page 103-104; 113pp; English.

XX The sequence represents the coding sequence of molecule for disease
 XX detection and treatment, mdc14, shown by computer analysis to be similar
 CC to Src homology domain family of proteins. The sequence may be used for
 CC somatic or germline gene therapy. Gene therapy may be performed to: (i)
 CC correct genetic deficiency such as in severe combined immunodeficiency
 CC syndrome associated with adenosine deaminase (ADA) deficiency, cystic
 CC fibrosis, thalassemias, familial hypercholesterolaemia and haemophilia
 CC caused by factor VIII or factor IX deficiencies; (ii) express a
 CC conditional lethal gene product (such as in the case of cancers which
 CC result from unregulated cell proliferation); (iii) express a protein
 CC which affords protection against intracellular parasites (for example,
 CC human retroviruses such as HIV, hepatitis B or C, fungal parasites such
 CC as Candida albicans and Paracoccidioides brasiliensis, and protozoal
 CC parasites such as Plasmodium falciparum and Trypanosoma brasiliensis).

XX Sequence 2109 BP; 545 A; 538 C; 562 G; 464 T; 0 other;

Query Match 23.2%; Score 39; DB 22; Length 2109;
 Best Local Similarity 54.5%; Pred. No. 0.053;
 Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

OY 25 TTCCCGCAGGTGGCCGCCGAGCTGTGAGACTCGGAGGCAATTACATGTC 84
 DB 504 TACCCGTCTCTGACATGAGCCCCGATATTCGCGAGGGAGAACTGCTGTATT 563
 OY 85 TCTGAGATGAGAGACTGTGAGAGCTGTGAGACTCTAGGAGAGATTAACATC 144
 DB 564 TCTGATGAAGGGGCTGTGTGGAAGCTATTCTTACAGCACTGTGAGAGATTACATC 623
 OY 145 CCGAGCTCCAGTGGCCAAAGT 167
 DB 624 CTTGGAATATGTGTGCCAGAT 646

RESULT 10
 ABR83738
 ID ABR83738 standard; cDNA; 2665 BP.

AC ABR83738;

DT 14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #309.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; peridontal disease;
 KW granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

PN WO200228999-A2.

PD 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

PA (GENE-) GENE LOGIC INC.

PI Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;

DR WPI: 2002-435328/46.

PT Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as

PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity.

PS Claim 1, SEQ ID No 309, 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC or allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome, renal
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2665 BP, 736 A, 617 C, 689 G, 623 T, 0 other:

QY Query Match 23.2%; Score 39; DB 24; Length 2665;

Best Local Similarity 54.5%; Pred. No. 0.055;

Matches: 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 25 TTCCGCGAGGTGACCCGCGAGGTGCGAGATCGCGAGGACATTGACCATGTC 84

Db 138 TACCGTCTCTGATCATCAGCCCGCGATTTCCGCGAGGAGAACTCGTGATTT 197

QY 85 TCTGAGATGAGACTGTGTGACGCTGTCTTAAGTCTCAGGCGAGAGATTAATC 144

Db 198 TCTGATGAGAGGGGCTGTGTGAGAAAGCTATTCTTTCAGCATGTGTCGAGAGATTAATC 257

QY 145 CCCAGGCTCCAGCTGCGCAAGT 167

Db 258 CTTGAGATATGTGTGGCCAGAT 280

RESULT 11

ABL65189

ID ABL65189 standard; DNA: 2665 BP.

XX ABL65189;

DT 15-MAY-2002 (first entry)

XX Lung cancer related gene sequence SEQ ID NO:3526.
DE Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; db.

XX Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-209473P.

XX 05-JUN-2000; 2000US-209531P.

XX 18-SEP-2000; 2000US-233133P.

XX 18-SEP-2000; 2000US-233137P.

XX 20-SEP-2000; 2000US-234009P.

XX 20-SEP-2000; 2000US-234034P.

XX 20-SEP-2000; 2000US-234052P.

XX 22-SEP-2000; 2000US-234509P.

XX 22-SEP-2000; 2000US-234567P.

XX 25-SEP-2000; 2000US-234923P.

XX 25-SEP-2000; 2000US-234924P.

XX 25-SEP-2000; 2000US-235077P.

XX 25-SEP-2000; 2000US-235082P.

XX 25-SEP-2000; 2000US-235134P.

XX 25-SEP-2000; 2000US-235280P.

XX 25-SEP-2000; 2000US-235637P.

XX 26-SEP-2000; 2000US-235638P.

XX 27-SEP-2000; 2000US-235711P.

XX 27-SEP-2000; 2000US-235720P.

XX 27-SEP-2000; 2000US-235840P.

XX 27-SEP-2000; 2000US-235863P.

XX 28-SEP-2000; 2000US-236028P.

XX 28-SEP-2000; 2000US-236032P.

XX 28-SEP-2000; 2000US-236033P.

XX 28-SEP-2000; 2000US-236034P.

XX 28-SEP-2000; 2000US-236109P.

XX 28-SEP-2000; 2000US-236111P.

XX 29-SEP-2000; 2000US-236842P.

XX 29-SEP-2000; 2000US-236891P.

XX 02-OCT-2000; 2000US-237172P.

XX 02-OCT-2000; 2000US-237173P.

XX 02-OCT-2000; 2000US-237278P.

XX 02-OCT-2000; 2000US-237294P.

XX 02-OCT-2000; 2000US-237295P.

XX 02-OCT-2000; 2000US-237316P.

XX 03-OCT-2000; 2000US-237425P.

XX 03-OCT-2000; 2000US-237598P.

XX 03-OCT-2000; 2000US-237604P.

XX 03-OCT-2000; 2000US-237606P.

XX 03-OCT-2000; 2000US-237608P.

XX 01-NOV-2000; 2000US-244867P.

XX 01-NOV-2000; 2000US-245084P.

XX (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S,
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX Claim 1; SEQ ID 3526; 44pp; English.

XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in

expression is indicative of anti-neoplastic activity. (II) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, CC oesophageal, ovarian, kidney, prostate or pancreatic cancer, CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumor.

Sequence 2665 BP; 736 A; 617 C; 689 G; 623 T; 0 other;

Query Match 23.2%; Score 39; DB 24; Length 2665;
Best Local Similarity 54.5%; Pred. No. 0.055;

Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Db 25 TTCCGGCAGCTGCGCCGCGAGCTGCTGAGCTGCGGAGCCATTGACATCGTC 84
138 TACCCGCTCTCTGACATCAAGCCCGCATTTCCGCCAGGAGAAACGTGGTGTATT 197

Qy 85 TCTGAGATGAGACTGTGTGACGCTCTCTGAACTCTCAGCAGAGATTAACATC 144
Db 198 TCTGATGAGGGGGCTGTGGAAGCTATTCTTACCTGCTGAGAGATTAACATC 257

Qy 145 CCCAGCTCCAGCTGGCCAAAGT 167
Db 258 CCGTGAATATGTGTGCGCAGAGT 280

RESULT 12

AAZ46491
ID AAZ46491 standard; DNA; 2032 BP.

XX AAZ46491;

AC 13-MAR-2000 (first entry)

DE PKA substrate, Src-family protein encoding DNA.

KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;

KW Kinase substrate; immunosuppressive disorder; proliferative disease;

KW HIV infection; AIDS; immunodeficiency; autoimmune disease;

XX systemic lupus erythematosus; Src-family; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Claim 22; Page 94-95; 11pp; English.

PS The invention provides a novel method of altering the activity of the
XX protein kinase A (PKA) signaling pathway in a cell that comprises
XX altering the extent of phosphorylation of one or more PKA substrates, or
XX kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
XX compositions containing a nucleic acid molecule that encodes a PKA
XX substrate, or fragment, precursor or functionally equivalent variant,
XX where the sequence is modified to alter its susceptibility to
XX phosphorylation by PKA can be used for treating a disorder exhibiting
XX abnormal PKA signaling activity, immunosuppressive disorders or
XX infection, AIDS, common variable immunodeficiency or cancers. Conditions
XX in which upregulation of the PKA pathway is required, such as autoimmune
XX disease, e.g. systemic lupus erythematosus, may also be treated. The
XX present sequence represents a DNA sequence encoding a PKA substrate,
XX wherein the substrate is in the Src-family, preferably Lck, Fyn, Src,
XX Yes, Fgr, Lyn, Hck, Blk, Yrk, C-trl, Fyk, Src-1 or Src-2.

Sequence 2032 BP; 450 A; 576 C; 584 G; 422 T; 0 other;

Query Match 20.5%; Score 34.4; DB 21; Length 2032;
Best Local Similarity 51.3%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 76;

Qy 11 TGCCCTGGGCGAGTTCCCGCAGGTGCGCCGCGAGCTTCTGCTGAGACTCGGGAGC 70
Db 251 TCCCTGTGACAGCTATGAGCCCTCTCAGCAGATCTGGGCTTGAAGAGGGGAGC 310

Qy 71 CATTGACATGCTCTGAGATGAGACTGTGAGCGTGTCTGAACTCTCAGGCA 130
Db 311 CACTCCGATCTCTGAGCAGAGCGGCGAGTGTGAAAGGCGCAGTCCCTGACACAGGGCC 370

Qy 131 GAGAGTATTAACATCCCGCAGCGCTCCACGTGGCCAAAG 166
Db 371 AGGAGGCTTCAATCCCTTCAATTTTGTGGCCAAAG 406

RESULT 13

AB31398/C
ID AB31398 standard; DNA; 577 BP.

XX AB31398;

AC 23-JAN-2002 (first entry)

DE Probe #9864 for gene expression analysis in human heart cell sample.

KW Human; gene expression; heart; microarray; vascular system; probe;

KW Cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease; ss.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

PT Altering the activity of protein kinase signaling pathways, used for
PT treating immunosuppressive disorders, e.g. AIDS, proliferative
PT disorders, e.g. cancers or autoimmune diseases -

PA (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX

DR WPI: 2001-488897/53.

XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -

PS Claim 1; SEQ ID No 9864; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

8Q Sequence 577 BP; 105 A; 197 C; 164 G; 111 T; 0 other;

Query Match 19.6%; Score 33; DB 22; Length 577;
Best Local Similarity 54.5%; Pred. No. 2.4;

Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 11 TGGCCTGGGAGTTCCCGGAGGTGGCCCGGAGCTGCTGAGACTCGGGAGC 70

Db 234 TGACCTTGCTGCTTTGCGGCCAGGTGGGAGCTGTGGGATCTCGAGCTCAGTCT 175

Qy 71 CATTGACCATGCTCTCTGAGATGAGACTGTGAGCGTCTGTGAGTCTCAGGCA 130

Db 174 CACCCGAGGATGAGAGGAGCTGTGAGTTCAAGGAGAGGCTCCGCTCAGCCA 115

Qy 131 G 131
Db 114 G 114

RESULT 14

AI44415/C

ID AI44415 standard; DNA; 577 BP.

AC AI44415;

DT 17-OCT-2001 (first entry)

DE Probe #13101 used to measure gene expression in human placenta sample.

KW Probe; microarray; human; placenta; antenatal diagnosis;

OS genetic disorder; ss.

XX Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0600408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR,

XX WPI: 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -

PS Claim 25; SEQ ID No 13101; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.

8Q Sequence 577 BP; 105 A; 197 C; 164 G; 111 T; 0 other;

Query Match 19.6%; Score 33; DB 22; Length 577;
Best Local Similarity 54.5%; Pred. No. 2.4;

Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 11 TGGCCTGGGAGTTCCCGGAGGTGGCCCGGAGCTGCTGAGACTCGGGAGC 70

Db 234 TGACCTTGCTGCTTTGCGGCCAGGTGGGAGCTGTGGGATCTCGAGCTCAGTCT 175

Qy 71 CATTGACCATGCTCTCTGAGATGAGACTGTGAGCGTCTGTGAGTCTCAGGCA 130

Db 174 CACCCGAGGATGAGAGGAGCTGTGAGTTCAAGGAGAGGCTCCGCTCAGCCA 115

Qy 131 G 131
Db 114 G 114

RESULT 15

AAT70377

ID AAT70377 standard; cDNA; 3311 BP.

AC AAT70377;

DT 15-DEC-1997 (first entry)

DE Cytohesin 1.

KW Cytohesin 1; cytohesin 2; cytohesin PH; T-lymphocyte; wound healing;

KW immune system; Pleckstrin; ss.

OS Homo sapiens.

PN EP763597-A2.

PD 19-MAR-1997.

PF 09-SEP-1996; 96EP-0114413.

PR 14-SEP-1995; 95DE-4034120.

PR (FARH) HOECHST AG.

PA Kolanus W, Schiller B, Ostner B;

PI WPI: 1997-167789/16.

PR P-PSDB; AAW18782.

XX Cytohesin-2 peptide and use of cytohesin PH peptide - for regulation

XX of T-lymphocyte activation

PT

XX Disclosure; Page 19-20; 30pp; German.

PS
CC The cytohesin 2 peptide (AAW18783) can be used for regulation
CC of T-lymphocyte activation. Cytohesin 2 and cytohesin PH peptides
CC can be used to modulate inflammation, promote wound healing,
CC suppress the immune system, esp. during organ transplantation,
CC inhibit metastasis of hematopoietic tumours and treat
CC arteriosclerosis. Cytohesin PH peptides comprise at least part
CC of the cytohesin 1 sequence, esp. amino acids 258-398 (AAT70377).
CC The PH peptides are Pleckstrin homology domains found in several
CC proteins.

SQ Sequence 3311 BP; 784 A; 820 C; 953 G; 754 T; 0 other;

Query Match 19.6%; Score 33; DB 18; Length 3311;

Best Local Similarity 52.6%; Pred. No. 3.5;

Matches 72; Conservative 0; Mismatches 65; Indels 0; Caps 0;

QY 30 GGCAGGTGGCCGCCGAGCTGTGCTGAGACTCGGGAGCCGACATGACCATGCTCTCA 89
DB 1927 GGGCAGAGGCCCTCAGTGAAGCCTCAAGACGACAGTCAAGTGGGGCTGCTGCGG 1986
QY 90 GGATGAGACTGTGTGACGCTGTCTGAAGTTCAGGACAGAGTATPACATCCCAAG 149
DB 1987 GGTGCGAGTGGGAGAGGCTGCAAGTCCGGCATCTCCGGAGTGTCTTTCATCCCAAG 2046
QY 150 GGTCCAGTGGCCCAAG 166
DB 2047 TGCTTGGAGGCCGAG 2063

Search completed: March 30, 2003, 00:48:28
Job time : 50.5859 secs